

The topologies are constructed considering all the certain transmembrane domains, but either including or excluding each of the putative ones. The resulting structures are shown in the text result window, but they are sorted before being displayed as a diagram. For the AMPHI algorithm, only the topology including all the transmembrane segments is considered.

The topologies are ranked according to their degree of bias in the distribution of positively charged residues (Arg and Lys). The rationale behind this ranking is that the correct structure should have the largest charge bias, since any structure with an incorrect number of segments would have one or more polar domains misplaced.

A number appears in the bottom-right corner. This number serves to locate this structure among those displayed in the text result window.